

SEQUENCE LISTING

<110> BUNEMANN, MORITZ
VILARDAGA, JEAN PIERRE
HOFFMAN, CARSTEN
LOHSE, MARTIN JOHANNES

<120> MILLISECOND ACTIVATION SWITCH FOR SEVEN-TRANSMEMBRANE PROTEINS

<130> VOSS:008US

<140> 10/538985

<141> 2005-06-15

<150> DE 102 59 874.6

<151> 2002-12-19

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<151> 2002-12-19

<150> EP 03 00 4394.7

<151> 2003-03-03

<160> 46

<170> PatentIn version 3.1

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<212> DNA

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Val	Pro	Pro	Ser	Arg	Arg	Gly	Pro	Asp	Ala	Cys	Ser	Ala	Pro	Pro	Gly	245	250	255	
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260		265		270
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Pro Gly Glu Pro Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp	290	295	300	
Leu Glu Glu Ser Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro	305	310	315	320
Arg Arg Pro Asp Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser	325	330	335	
Gln Val Lys Pro Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala	340	345	350	
Gly Pro Gly Ala Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly	355	360	365	
Ala Lys Ala Ser Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe	370	375	380	
Thr Phe Val Leu Ala Val Val Ile Gly Val Phe Val Val Cys Trp Phe	385	390	395	400
Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val Gly Cys Pro Val Pro	405	410	415	
Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly Tyr Cys Asn Ser Ser	420	425	430	
Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His Asp Phe Arg Arg Ala	435	440	445	
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<212> DNA

<213> homo sapiens

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<212> PRT

<213> homo sapiens

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 35 40 45

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
 50 55 60

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
 65 70 75 80

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
 85 90 95

Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp
 100 105 110

Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala
 115 120 125

Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala
 130 135 140

Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His
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Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn
165 170 175

Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
180 185 190

Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile
195 200 205

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210 215 220

His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys
225 230 235 240

Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu
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Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala
260 265 270

Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe
275 280 285

Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
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Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
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Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp
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Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
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Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val

370

375

380

Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg
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Ser Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn
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Ser Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly
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Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
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Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
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Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
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Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
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Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
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Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
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<211> 1238

<212> DNA

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<212> PRT

<213> homo sapiens

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Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr
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Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala
65 70 75 80

Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala
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Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn
100 105 110

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp
115 120 125

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn
130 135 140

Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu
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Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met
165 170 175

Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu Met

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Phe	Ala	Leu	Cys	Trp	Leu	Pro	Leu	His	Ile	Ile	Asn	Cys	Phe	Thr	Phe
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<213> artificial sequence

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<211> 239

<212> PRT

<213> artificial sequence

<220>

<223> eCFP (enhanced CFP) amino acid sequence

<400> 8

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile
35 40 45

Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr
50 55 60

Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys
65 70 75 80

Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu
85 90 95

Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu
100 105 110

Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly
115 120 125

Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr
130 135 140

Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn
145 150 155 160

Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser
165 170 175

Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly
180 185 190

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu
195 200 205

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
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Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
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<212> PRT
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<223> YFP amino acid sequence

<400> 10

Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu

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Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile	35	40	45
Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr	50	55	60
Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys	65	70	75
Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu	85	90	95
Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu	100	105	110
Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly	115	120	125
Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr	130	135	140
Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn	145	150	155
Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser	165	170	175
Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly	180	185	190
Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu	195	200	205
Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe	210	215	220
Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	225	230	235

<210> 11

<211> 2457

<212> DNA

<213> artificial sequence

<220>

<223> alpha2a adrenergic receptor-cam cDNA sequence

<400> 11

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ggcaacagca gctggaacgg gaccgaagcg cccggaggcg gcacccgagc cacccttac	120
tccctgcagg tgacactgac gctggtttgc ctggctggcc tgctcatgct gttcacagta	180
tttggaacg tgctggttat tatcgcggtg ttcaccagtc gcgcgctcaa agctcccaa	240
aacctcttcc tgggtgtcct ggcctcagcg gacatcctgg tggccacgct ggtcattccc	300
ttttctttgg ccaacgaggt tatgggttac tggtactttg gtaagggtgtg gtgtgagatc	360
tatttggtc tcgacgtgct cttttgcacg tcgtccatag tgcacctgtg cgccatcagc	420
cttgaccgct actggtccat cacgcaggcc atcgagtaca acctgaagcg cagccgcgt	480
cgcataagg ccatcattgt caccgtgtgg gtcattctcg ctgtcatctc cttcccgcca	540
ctcatctcca tagagaagaa gggcgctggc ggcgggcagc agccggccga gccaaagtgc	600
aagatcaacg accagaagtg gtatgtcatc tcctcgtcca tcggttcctt cttegcgcct	660
tgctcatca tgatcctggt ctacgtgctg atttaccaga tcgccaagcg tcgcacccgc	720
gtgcctcca gccgccggg tccggacgcc atggtgagca agggcgagga gctgttcacc	780
ggggtggtgc ccatcctggt cgagctggac ggcgacgtaa acggccacaa gttcagcgtg	840
tccggcgagg gcgagggcga tgccacctac ggcaagctga ccctgaagtt catctgcacc	900
accggcaagc tgcccgtgcc ctggcccacc ctctgaccca ccttcggcta cggcctgcag	960
tgcttcgccc gctaccccga ccacatgaag cagcacgact tcttcaagtc cgccatgccc	1020
gaaggctacg tccaggagcg caccatcttc ttcaaggacg acggcaacta caagaccgcg	1080
gccgaggtga agttcgaggg cgacaccctg gtgaaccgca tcgagctgaa gggcatcgac	1140
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gacggccccg tgctgctgcc cgacaaccac tacctgagct accagtccgc cctgagcaaa	1380
gaccccaacg agaagcgcga tcacatggtc ctgctggagt tcgtgaccgc cgccgggatac	1440
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ttcacgttcg tgctggcggg ggtgatcggc gtgttcgtgg tgtgttggtt tccgttcttt	1560
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gacgtaaacg gccacaagtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc	1860
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ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc	2220
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cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgccga caaccactac	2340
ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg	2400
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<210> 12

<211> 818

<212> PRT

<213> artificial sequence

<220>

<223> alpha 2a adrenergic receptor-cam "chameleon" amino acid sequence

<400> 12

Met Gly Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser Met Gly Ser Leu
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Gln Pro Asp Ala Gly Asn Ser Ser Trp Asn Gly Thr Glu Ala Pro Gly
20 25 30

Gly Gly Thr Arg Ala Thr Pro Tyr Ser Leu Gln Val Thr Leu Thr Leu
35 40 45

Val Cys Leu Ala Gly Leu Leu Met Leu Phe Thr Val Phe Gly Asn Val
50 55 60

Leu Val Ile Ile Ala Val Phe Thr Ser Arg Ala Leu Lys Ala Pro Gln
65 70 75 80

Asn Leu Phe Leu Val Ser Leu Ala Ser Ala Asp Ile Leu Val Ala Thr
85 90 95

Leu Val Ile Pro Phe Ser Leu Ala Asn Glu Val Met Gly Tyr Trp Tyr
100 105 110

Phe Gly Lys Val Trp Cys Glu Ile Tyr Leu Ala Leu Asp Val Leu Phe
115 120 125

Cys Thr Ser Ser Ile Val His Leu Cys Ala Ile Ser Leu Asp Arg Tyr
130 135 140

Trp Ser Ile Thr Gln Ala Ile Glu Tyr Asn Leu Lys Arg Thr Pro Arg
145 150 155 160

Arg Ile Lys Ala Ile Ile Val Thr Val Trp Val Ile Ser Ala Val Ile
165 170 175

Ser Phe Pro Pro Leu Ile Ser Ile Glu Lys Lys Gly Ala Gly Gly Gly
180 185 190

Gln Gln Pro Ala Glu Pro Ser Cys Lys Ile Asn Asp Gln Lys Trp Tyr
195 200 205

Val Ile Ser Ser Ser Ile Gly Ser Phe Phe Ala Pro Cys Leu Ile Met
210 215 220

Ile Leu Val Tyr Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg
225 230 235 240

Val Pro Pro Ser Arg Arg Gly Pro Asp Ala Met Val Ser Lys Gly Glu
245 250 255

Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp
260 265 270

Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala
275 280 285

Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu
290 295 300

Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln
305 310 315 320

Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys
325 330 335

Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys
340 345 350

Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp
355 360 365

Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp
370 375 380

Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn
385 390 395 400

Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe
405 410 415

Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His
420 425 430

Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp
435 440 445

Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu
450 455 460

Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile
465 470 475 480

Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg Trp Arg Gly Arg Gln Asn
485 490 495

Arg Glu Lys Arg Phe Thr Phe Val Leu Ala Val Val Ile Gly Val Phe
500 505 510

Val Val Cys Trp Phe Pro Phe Phe Phe Thr Tyr Thr Leu Ile Ala Val
515 520 525

Gly Cys Pro Val Pro Ser Gln Leu Phe Asn Phe Phe Phe Trp Phe Gly
530 535 540

Tyr Cys Asn Ser Ser Leu Asn Pro Val Ile Tyr Thr Ile Phe Asn His
545 550 555 560

Asp Phe Arg Arg Ala Phe Lys Lys Ile Leu Cys Arg Gly Asp Arg Lys
565 570 575

Arg Ile Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
580 585 590

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
595 600 605

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
610 615 620

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
625 630 635 640

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
645 650 655

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
660 665 670

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr

675	680	685
Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu 690 695 700		
Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys 705 710 715 720		
Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys 725 730 735		
Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu 740 745 750		
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile 755 760 765		
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln 770 775 780		
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu 785 790 795 800		
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu 805 810 815		

Tyr Lys

<210> 13

<211> 2928

<212> DNA

<213> artificial sequence

<220>

<223> PTH receptor-cam "chameleon" 8 cDNA sequence

<400> 13

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tccgcgtacg cgctggtgga tgcagatgac gtcattgacta aagaggaaca gatcttctg	120

ctgcaccgtg	ctcaggccca	gtgcgaaaaa	cggctcaagg	aggtcctgca	gaggccagcc	180
agcataatgg	aatcagacaa	gggatggaca	tctgcgcca	catcaggga	gcccaggaaa	240
gataaggcat	ctgggaagct	ctaccctgag	tctgaggagg	acaaggaggc	acccactggc	300
agcaggtacc	gagggcgccc	ctgtctgccc	gaatgggacc	acatcctgtg	ctggccgctg	360
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tacatccaca	tgcacctgtt	cctgtccttc	atgctgcgcg	ccgtgagcat	cttcgtcaag	720
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ctgcgcgcca	tcgcccaggc	gccccgcgcg	cctgccaccg	ccgctgccgg	ctacgcgggc	840
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tccgccctga gcaaagaccc caacgagaag cgcgatcaca tggtcctgct ggagttcgtg	1860
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cagtaccgga agctgctcaa atccacgctg gtgctcatgc ccctctttgg cgtccactac	1980
attgtcttca tggccacacc atacaccgag gtctcagga cgctctggca agtccagatg	2040
cactatgaga tgctcttcaa ctccctccag ggattttttg tcgcaatcat atactgtttc	2100
tgcaatggcg aggtacaagc tgagatcaag aaatcttggg gccgctggac actggcactg	2160
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ggcgaggagc tggtcaccgg ggtggtgccc atcctggtcg agctggacgg cgacgtaaac	2280
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gagctgaagg gcatcgactt caaggaggac ggcaacatcc tggggcacia gctggagtac	2640
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aacttcaaga tccgccacia catcgaggac ggcagcgtgc agctcgccga ccactaccag	2760
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cagtccgcc tgagcaaaga cccaacgag aagcgcgatc acatggtcct gctggagttc	2880
gtgaccgccg ccgggatcac tctcggcatg gacgagctgt acaagtaa	2928

<210> 14

<211> 975

<212> PRT

<213> artificial sequence

<220>

<223> PTH receptor-cam8 "chameleon" amino acid sequence

<400> 14

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20 25 30

Thr Lys Glu Glu Gln Ile Phe Leu Leu His Arg Ala Gln Ala Gln Cys
35 40 45

Glu Lys Arg Leu Lys Glu Val Leu Gln Arg Pro Ala Ser Ile Met Glu
50 55 60

Ser Asp Lys Gly Trp Thr Ser Ala Ser Thr Ser Gly Lys Pro Arg Lys
65 70 75 80

Asp Lys Ala Ser Gly Lys Leu Tyr Pro Glu Ser Glu Glu Asp Lys Glu
85 90 95

Ala Pro Thr Gly Ser Arg Tyr Arg Gly Arg Pro Cys Leu Pro Glu Trp
100 105 110

Asp His Ile Leu Cys Trp Pro Leu Gly Ala Pro Gly Glu Val Val Ala
115 120 125

Val Pro Cys Pro Asp Tyr Ile Tyr Asp Phe Asn His Lys Gly His Ala
130 135 140

Tyr Arg Arg Cys Asp Arg Asn Gly Ser Trp Glu Leu Val Pro Gly His
145 150 155 160

Asn Arg Thr Trp Ala Asn Tyr Ser Glu Cys Val Lys Phe Leu Thr Asn
165 170 175

Glu Thr Arg Glu Arg Glu Val Phe Asp Arg Leu Gly Met Ile Tyr Thr
180 185 190

Val Gly Tyr Ser Val Ser Leu Ala Ser Leu Thr Val Ala Val Leu Ile
195 200 205

Leu Ala Tyr Phe Arg Arg Leu His Cys Thr Arg Asn Tyr Ile His Met
210 215 220

His Leu Phe Leu Ser Phe Met Leu Arg Ala Val Ser Ile Phe Val Lys
225 230 235 240

Asp Ala Val Leu Tyr Ser Gly Ala Thr Leu Asp Glu Ala Glu Arg Leu
245 250 255

Thr Glu Glu Glu Leu Arg Ala Ile Ala Gln Ala Pro Pro Pro Pro Ala
260 265 270

Thr Ala Ala Ala Gly Tyr Ala Gly Cys Arg Val Ala Val Thr Phe Phe
275 280 285

Leu Tyr Phe Leu Ala Thr Asn Tyr Tyr Trp Ile Leu Val Glu Gly Leu
290 295 300

Tyr Leu His Ser Leu Ile Phe Met Ala Phe Phe Ser Glu Lys Lys Tyr
305 310 315 320

Leu Trp Gly Phe Thr Val Phe Gly Trp Gly Leu Pro Ala Val Phe Val
325 330 335

Ala Val Trp Val Ser Val Arg Ala Thr Leu Ala Asn Thr Gly Cys Trp
340 345 350

Asp Leu Ser Ser Gly Asn Lys Lys Trp Ile Ile Gln Val Pro Ile Leu
355 360 365

Ala Ser Ile Val Leu Asn Phe Ile Leu Phe Ile Asn Ile Val Arg Val
370 375 380

Leu Ala Thr Lys Leu Arg Glu Thr Asn Ala Gly Met Val Ser Lys Gly
385 390 395 400

Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly
405 410 415

Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp
420 425 430

Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys
435 440 445

Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val
450 455 460

Gln Cys Phe Ser Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe
465 470 475 480

Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe
485 490 495

Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly
500 505 510

Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu
515 520 525

Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His
530 535 540

Asn Val Tyr Ile Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn
545 550 555 560

Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp
565 570 575

His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro
580 585 590

Asp Asn His Tyr Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn
595 600 605

Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly
610 615 620

Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys Arg Cys Asp Thr Arg Gln
625 630 635 640

Gln Tyr Arg Lys Leu Leu Lys Ser Thr Leu Val Leu Met Pro Leu Phe
645 650 655

Gly Val His Tyr Ile Val Phe Met Ala Thr Pro Tyr Thr Glu Val Ser
660 665 670

Gly Thr Leu Trp Gln Val Gln Met His Tyr Glu Met Leu Phe Asn Ser
675 680 685

Phe Gln Gly Phe Phe Val Ala Ile Ile Tyr Cys Phe Cys Asn Gly Glu

690				695				700							
Val 705	Gln	Ala	Glu	Ile	Lys 710	Lys	Ser	Trp	Ser	Arg 715	Trp	Thr	Leu	Ala	Leu 720
Asp	Phe	Lys	Arg	Lys 725	Ala	Arg	Ser	Gly	Ser 730	Ser	Ser	Tyr	Ser	Tyr 735	Gly
Met	Val	Ser	Lys 740	Gly	Glu	Glu	Leu	Phe 745	Thr	Gly	Val	Val	Pro 750	Ile	Leu
Val	Glu	Leu 755	Asp	Gly	Asp	Val	Asn 760	Gly	His	Lys	Phe 765	Ser	Val	Ser	Gly
Glu	Gly 770	Glu	Gly	Asp	Ala	Thr 775	Tyr	Gly	Lys	Leu	Thr 780	Leu	Lys	Phe	Ile
Cys 785	Thr	Thr	Gly	Lys	Leu 790	Pro	Val	Pro	Trp	Pro 795	Thr	Leu	Val	Thr	Thr 800
Phe	Gly	Tyr	Gly	Leu 805	Gln	Cys	Phe	Ala	Arg 810	Tyr	Pro	Asp	His	Met 815	Lys
Gln	His	Asp	Phe 820	Phe	Lys	Ser	Ala	Met 825	Pro	Glu	Gly	Tyr	Val 830	Gln	Glu
Arg	Thr 835	Ile	Phe	Phe	Lys	Asp	Asp 840	Gly	Asn	Tyr	Lys	Thr 845	Arg	Ala	Glu
Val 850	Lys	Phe	Glu	Gly	Asp	Thr 855	Leu	Val	Asn	Arg	Ile 860	Glu	Leu	Lys	Gly
Ile 865	Asp	Phe	Lys	Glu	Asp	Gly 870	Asn	Ile	Leu	Gly 875	His	Lys	Leu	Glu	Tyr 880
Asn	Tyr	Asn	Ser	His 885	Asn	Val	Tyr	Ile	Met 890	Ala	Asp	Lys	Gln	Lys 895	Asn
Gly	Ile	Lys	Val 900	Asn	Phe	Lys	Ile	Arg 905	His	Asn	Ile	Glu	Asp 910	Gly	Ser
Val	Gln	Leu 915	Ala	Asp	His	Tyr	Gln 920	Gln	Asn	Thr	Pro	Ile 925	Gly	Asp	Gly

Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu
 930 935 940

Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe
 945 950 955 960

Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
 965 970 975

<210> 15

<211> 2361

<212> DNA

<213> artificial sequence

<220>

<223> A2A-CFP14/10-YFP-C33 cDNA sequence; A2A "chameleon"

<400> 15

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ccctttgcc taccatcag caccgggttc tgcgtgcct gccacggctg cctcttcatt	240
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ctaggttga acaactgcgg tcagccaaag gagggcaaga accactcca gggctgcggg	480
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aacgtctata tcaccgccga caagcagaag aacggcatca aggccaactt caagatccgc	1140
cacaacatcg aggacggcag cgtgcagctc gccgaccact accagcagaa ccccccatc	1200
ggcgacggcc ccgtgctgct gcccgacaac cactacctga gcaccagtc cgccctgagc	1260
aaagacccca acgagaagcg cgatcacatg gtctgtctgg agttcgtgac cgccgcccgg	1320
atcactctcg gcatggacga gctgtacaag cttcagaagg aggtccatgc tgccaagtca	1380
ctggccatca ttgtggggct ctttgccctc tgctggctgc ccctacacat catcaactgc	1440
ttcactttct tctgccccga ctgcagccac gcccctctct ggctcatgta cctggccatc	1500
gtcctctccc acaccaattc ggttgtgaat cccttcatct acgcctaccg tatccgcgag	1560
ttccgccaga ctttcgcaa gatcattcgc agccacgtcc tgaggcagca agaacctttc	1620
aaggcagctg gcaccagtc cggggtcgtg agcaaggcg aggagctgtt caccggggtg	1680
gtgcccaccc tggtcgagct ggacggcgac gtaaaccggc acaagttcag cgtgtccggc	1740
gagggcgagg gcgatgccac ctacggcaag ctgaccctga agttcatctg caccaccggc	1800
aagctgcccg tgccctggcc caccctcgtg accaccttcg gctacggcct gcagtgttc	1860
gccgctacc ccgaccacat gaagcagcac gacttcttca agtccgccat gccgaaggc	1920
tacgtccagg agcgcacat cttcttcaag gacgacggca actacaagac ccgcgccgag	1980
gtgaagttcg agggcgacac cctggtgaac cgcacgagc tgaaggcat cgacttcaag	2040
gaggacggca acatcctggg gcacaagctg gagtacaact acaacagcca caacgtctat	2100
atcatggccg acaagcagaa gaacggcatc aaggtgaact tcaagatccg ccacaacatc	2160
gaggacggca gcgtgcagct cgccgaccac taccagcaga acaccccat cggcgacggc	2220
cccgtgctgc tgcccgacaa ccactacctg agctaccagt ccgccctgag caaagacccc	2280
aacgagaagc gcgatcacat ggtcctgctg gagttcgtga ccgccgccgg gatcactctc	2340
ggcatggacg agctgtacaa g	2361

<210> 16

<211> 784

<212> PRT

<213> artificial sequence

<220>

<223> A2A-CFP14/10-YFP-C33 amino acid sequence; "A2A chameleon"

<400> 16

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Ser Leu Ala
35 40 45

Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile Thr
50 55 60

Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile Ala
65 70 75 80

Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu Ala
85 90 95

Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr Asn
100 105 110

Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys Trp
115 120 125

Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn Asn
130 135 140

Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly Glu
145 150 155 160

Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr Met
165 170 175

Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu Met

180	185	190
Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu Lys		
195	200	205
Gln Met Glu Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro		
210	215	220
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val		
225	230	235
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys		
	245	250
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val		
	260	265
Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His		
	275	280
Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val		
	290	295
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg		
305	310	315
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu		
	325	330
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu		
	340	345
Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln		
	355	360
Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg His Asn Ile Glu Asp		
	370	375
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly		
385	390	395
Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser		
	405	410
		415

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
420 425 430

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
435 440 445

Lys Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val
450 455 460

Gly Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe
465 470 475 480

Thr Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr
485 490 495

Leu Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile
500 505 510

Tyr Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile
515 520 525

Arg Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr
530 535 540

Ser Ala Arg Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
545 550 555 560

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
565 570 575

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
580 585 590

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
595 600 605

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
610 615 620

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
625 630 635 640

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
645 650 655

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
660 665 670

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
675 680 685

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
690 695 700

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
705 710 715 720

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
725 730 735

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
740 745 750

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
755 760 765

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
770 775 780

<210> 17

<211> 477

<212> DNA

<213> Mouse

<400> 17
gtgcgtatatt accagatcgc caagcgtcgc acccgcgtgc ctcccagccg ccgggggtccg 60
gacgcctgtt ccgcgccgcc gggggggcgcc gatcgcaggc ccaacgggct gggcccgag 120
cgcggcgcgg gtcccacggg cgctgaggcg gagccgctgc ccaccagct taacggtgccc 180
ccggggggagc ccgcgcccgc cgggccccgc gatgggggatg cgctggacct agaggagagt 240
tcgtcgtccg agcacgccga gcggcccccg gggccccgca gaccgcaccg cggcccccca 300

gccaagggca agaccgggc gagtcaggtg aagccggggg acagtctgcc gcggcgcggg 360
 cccggggccg cggggccggg ggcttcgggg tccgggcacg gagaggagcg cggcgggggc 420
 gccaaagcgt cgcgctggcg cgggaggcaa aaccgggaga aacgcttcac gttcgtg 477

<210> 18

<211> 159

<212> PRT

<213> Mouse

<400> 18

Val Arg Ile Tyr Gln Ile Ala Lys Arg Arg Thr Arg Val Pro Pro Ser
 1 5 10 15

Arg Arg Gly Pro Asp Ala Cys Ser Ala Pro Pro Gly Gly Ala Asp Arg
 20 25 30

Arg Pro Asn Gly Leu Gly Pro Glu Arg Gly Ala Gly Pro Thr Gly Ala
 35 40 45

Glu Ala Glu Pro Leu Pro Thr Gln Leu Asn Gly Ala Pro Gly Glu Pro
 50 55 60

Ala Pro Ala Gly Pro Arg Asp Gly Asp Ala Leu Asp Leu Glu Glu Ser
 65 70 75 80

Ser Ser Ser Glu His Ala Glu Arg Pro Pro Gly Pro Arg Arg Pro Asp
 85 90 95

Arg Gly Pro Arg Ala Lys Gly Lys Thr Arg Ala Ser Gln Val Lys Pro
 100 105 110

Gly Asp Ser Leu Pro Arg Arg Gly Pro Gly Ala Ala Gly Pro Gly Ala
 115 120 125

Ser Gly Ser Gly His Gly Glu Glu Arg Gly Gly Gly Ala Lys Ala Ser
 130 135 140

Arg Trp Arg Gly Arg Gln Asn Arg Glu Lys Arg Phe Thr Phe Val

<211> 36

<212> PRT

<213> homo sapiens

<400> 22

Arg	Ile	Phe	Leu	Ala	Ala	Arg	Arg	Gln	Leu	Lys	Gln	Met	Glu	Ser	Gln
1				5				10					15		

Pro	Leu	Pro	Gly	Glu	Arg	Ala	Arg	Ser	Thr	Leu	Gln	Lys	Glu	Val	His
			20					25					30		

Ala	Ala	Lys	Ser
			35

<210> 23

<211> 369

<212> DNA

<213> homo sapiens

<400> 23

cgtatccgcg agttccgcca gaccttccgc aagatcattc gcagccacgt cctgaggcag	60
caagaacctt tcaaggcagc tggcaccagt gcccggtct tggcagctca tggcagtgac	120
ggagagcagg tcagcctccg tctcaacggc caccgccag gagtgtgggc caacggcagt	180
gctccccacc ctgagcggag gcccaatggc tatgccctgg ggctgggtgag tggagggagt	240
gcccaagagt cccaggggaa cacgggcctc ccagacgtgg agtccttag ccatgagctc	300
aagggagtgt gccagagcc ccctggccta gatgaccccc tggcccagga tggagcagga	360
gtgtcctga	369

<210> 24

<211> 102

<212> PRT

<213> homo sapiens

<400> 24

Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg Ser His
1 5 10 15

Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser Ala Arg
20 25 30

Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu Arg Leu
35 40 45

Asn Gly His Pro Pro Gly Val Trp Ala Asn Gly Ser Ala Pro His Pro
50 55 60

Glu Arg Arg Pro Asn Gly Tyr Ala Leu Gly Leu Val Ser Gly Gly Ser
65 70 75 80

Ala Gln Glu Ser Gln Gly Asn Thr Gly Leu Pro Asp Val Glu Leu Leu
85 90 95

Ser His Glu Leu Lys Gly
100

<210> 25

<211> 57

<212> DNA

<213> homo sapiens

<400> 25

accaagctgc gggagaccaa cgccggccgg tgtgacacac ggcagcagta ccggaag

57

<210> 26

<211> 19

<212> PRT

<213> homo sapiens

<400> 26

Thr Lys Leu Arg Glu Thr Asn Ala Gly Arg Cys Asp Thr Arg Gln Gln
 1 5 10 15

Tyr Arg Lys

<210> 27

<211> 393

<212> DNA

<213> homo sapiens

<400> 27
 gaggtacaag ctgagatcaa gaaatcttgg agccgctgga cactggcact ggacttcaag 60
 cgaaaggcac gcagcgggag cagcagctat agctacggcc ccatggtgtc ccacacaagt 120
 gtgaccaatg tcggcccccg tgtgggactc ggcttgcccc tcagcccccg cctactgccc 180
 actgccacca ccaacggcca ccctcagctg cctggccatg ccaagccagg gaccccagcc 240-
 ctggagaccc tcgagaccac accacctgcc atggctgctc ccaaggacga tgggttcctc 300
 aacggctcct gctcaggcct ggacgaggag gcctctgggc ctgagcggcc acctgcctg 360
 ctacaggaag agtgggagac agtcatgtga tga 393

<210> 28

<211> 129

<212> PRT

<213> homo sapiens

<400> 28

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
 1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
 20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
 35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
100 105 110

Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val
115 120 125

Met

<210> 29

<211> 264

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam7 amino acid sequence

<400> 29

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Met Val Ser Lys Gly Glu Glu
20 25 30

Leu Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val
35 40 45

Asn Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr
50 55 60

Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro
65 70 75 80

Val Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys
85 90 95

Phe Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser
100 105 110

Ala Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp
115 120 125

Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr
130 135 140

Leu Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly
145 150 155 160

Asn Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val
165 170 175

Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys
180 185 190

Ile Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr
195 200 205

Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn
210 215 220

His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys
225 230 235 240

Arg Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr
245 250 255

Leu Gly Met Asp Glu Leu Tyr Lys
260

<210> 30

<211> 270

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam9 amino acid sequence

<400> 30

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Met
20 25 30

Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile Leu Val
35 40 45

Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser Gly Glu
50 55 60

Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe Ile Cys
65 70 75 80

Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr Thr Phe
85 90 95

Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met Lys Gln
100 105 110

His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln Glu Arg
115 120 125

Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala Glu Val
130 135 140

Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys Gly Ile
145 150 155 160

Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu Tyr Asn
165 170 175

Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys Asn Gly

	180		185		190
Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly Ser Val	195	200	205		
Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp Gly Pro	210	215	220		
Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala Leu Ser	225	230	235	240	
Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu Phe Val	245	250	255		
Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys	260	265	270		

<210> 31

<211> 272

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam8 amino acid sequence

<400> 31

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala	1	5	10	15
Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr	20	25	30	
Gly Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile	35	40	45	
Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser	50	55	60	
Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe	65	70	75	80

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
85 90 95

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met
100 105 110

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
115 120 125

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
130 135 140

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
145 150 155 160

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
165 170 175

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
180 185 190

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
195 200 205

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
210 215 220

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
225 230 235 240

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
245 250 255

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
260 265 270

<210> 32

<211> 275

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam2 amino acid sequence

<400> 32

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
35 40 45

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
50 55 60

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
65 70 75 80

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
85 90 95

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
100 105 110

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
115 120 125

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
130 135 140

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
145 150 155 160

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
165 170 175

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
180 185 190

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
195 200 205

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
210 215 220

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
225 230 235 240

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
245 250 255

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
260 265 270

Leu Tyr Lys
275

<210> 33

<211> 289

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam5 amino acid sequence

<400> 33

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro
50 55 60

Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val
65 70 75 80

Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys
85 90 95

Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val
100 105 110

Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His
115 120 125

Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val
130 135 140

Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg
145 150 155 160

Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu
165 170 175

Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu
180 185 190

Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln
195 200 205

Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp
210 215 220

Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly
225 230 235 240

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser
245 250 255

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
260 265 270

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
275 280 285

Lys

<210> 34

<211> 325

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-caml amino acid sequence

<400> ` 34

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Met Val Ser Lys Gly Glu Glu Leu Phe Thr
85 90 95

Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His
100 105 110

Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys
115 120 125

Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp
130 135 140

Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg
145 150 155 160

Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro
165 170 175

Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn
180 185 190

Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn
195 200 205

Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu
210 215 220

Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met
225 230 235 240

Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His
245 250 255

Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn
260 265 270

Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu
275 280 285

Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His
290 295 300

Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met
305 310 315 320

Asp Glu Leu Tyr Lys
325

<210> 35

<211> 339

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam4 amino acid sequence

<400> 35

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
85 90 95

Asp Gly Phe Leu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val
100 105 110

Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe
115 120 125

Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr
130 135 140

Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr
145 150 155 160

Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro
165 170 175

Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly
180 185 190

Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys
195 200 205

Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile
210 215 220

Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His
225 230 235 240

Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp
245 250 255

Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile
260 265 270

Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro
275 280 285

Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr
290 295 300

Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val
305 310 315 320

Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu
325 330 335

Leu Tyr Lys

<210> 36

<211> 354

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam3 amino acid sequence

<400> 36

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
100 105 110

Gly Pro Glu Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
115 120 125

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser
130 135 140

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
145 150 155 160

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
165 170 175

Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp
180 185 190

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
195 200 205

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
210 215 220

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
225 230 235 240

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys

	245		250		255
Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys					
	260		265		270
Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu					
	275		280		285
Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile					
	290		295		300
Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln					
	305		310		315
Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu					
	325		330		335
Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu					
	340		345		350

Tyr Lys

<210> 37

<211> 368

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-cam10 amino acid sequence

<400> 37

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Ser Gly Ser Ser Ser Tyr Ser Tyr
20 25 30

Gly Pro Met Val Ser His Thr Ser Val Thr Asn Val Gly Pro Arg Val
35 40 45

Gly Leu Gly Leu Pro Leu Ser Pro Arg Leu Leu Pro Thr Ala Thr Thr
50 55 60

Asn Gly His Pro Gln Leu Pro Gly His Ala Lys Pro Gly Thr Pro Ala
65 70 75 80

Leu Glu Thr Leu Glu Thr Thr Pro Pro Ala Met Ala Ala Pro Lys Asp
85 90 95

Asp Gly Phe Leu Asn Gly Ser Cys Ser Gly Leu Asp Glu Glu Ala Ser
100 105 110

Gly Pro Glu Arg Pro Pro Ala Leu Leu Gln Glu Glu Trp Glu Thr Val
115 120 125

Met Met Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro Ile
130 135 140

Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Lys Phe Ser Val Ser
145 150 155 160

Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys Phe
165 170 175

Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val Thr
180 185 190

Thr Phe Gly Tyr Gly Leu Gln Cys Phe Ala Arg Tyr Pro Asp His Met
195 200 205

Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val Gln
210 215 220

Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg Ala
225 230 235 240

Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu Lys
245 250 255

Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu Glu
260 265 270

Tyr Asn Tyr Asn Ser His Asn Val Tyr Ile Met Ala Asp Lys Gln Lys
275 280 285

Asn Gly Ile Lys Val Asn Phe Lys Ile Arg His Asn Ile Glu Asp Gly
290 295 300

Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly Asp
305 310 315 320

Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Tyr Gln Ser Ala
325 330 335

Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu Glu
340 345 350

Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr Lys
355 360 365

<210> 38

<211> 518

<212> PRT

<213> artificial sequence

<220>

<223> PTHR-PTHR-FRETcontrol amino acid sequence

<400> 38

Glu Val Gln Ala Glu Ile Lys Lys Ser Trp Ser Arg Trp Thr Leu Ala
1 5 10 15

Leu Asp Phe Lys Arg Lys Ala Arg Met Val Ser Lys Gly Glu Glu Leu
20 25 30

Phe Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn
35 40 45

Gly His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr
50 55 60

Gly Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val
65 70 75 80

Pro Trp Pro Thr Leu Val Thr Thr Phe Gly Tyr Gly Leu Gln Cys Phe
85 90 95

Ala Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala
100 105 110

Met Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp
115 120 125

Gly Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu
130 135 140

Val Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn
145 150 155 160

Ile Leu Gly His Lys Leu Glu Tyr Asn Tyr Asn Ser His Asn Val Tyr
165 170 175

Ile Met Ala Asp Lys Gln Lys Asn Gly Ile Lys Val Asn Phe Lys Ile
180 185 190

Arg His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln
195 200 205

Gln Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His
210 215 220

Tyr Leu Ser Tyr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg
225 230 235 240

Asp His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu
245 250 255

Gly Met Asp Glu Leu Tyr Lys Ser Gly Ser Ser Ser Tyr Ser Tyr Gly
260 265 270

Pro Met Val Ser His Thr Ser Met Val Ser Lys Gly Glu Glu Leu Phe
275 280 285

Thr Gly Val Val Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly

290		295		300
His Lys Phe Ser Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly				
305		310		315 320
Lys Leu Thr Leu Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro				
	325		330	335
Trp Pro Thr Leu Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser				
	340		345	350
Arg Tyr Pro Asp His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met				
	355		360	365
Pro Glu Gly Tyr Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly				
	370		375	380
Asn Tyr Lys Thr Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val				
385		390		395 400
Asn Arg Ile Glu Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile				
	405		410	415
Leu Gly His Lys Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile				
	420		425	430
Thr Ala Asp Lys Gln Lys Asn Gly Ile Lys Ala Asn Phe Lys Ile Arg				
	435		440	445
His Asn Ile Glu Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln				
	450		455	460
Asn Thr Pro Ile Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr				
465		470		475 480
Leu Ser Thr Gln Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp				
	485		490	495
His Met Val Leu Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly				
	500		505	510
Met Asp Glu Leu Tyr Lys				
	515			

<210> 39

<211> 1737

<212> DNA

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C49 cDNA sequence

<400> 39

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atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc	120
accaactact ttgtggtgtc actggcgggc gccgacatcg cagtgggtgt gctcgccatc	180
ccctttgcc taccatcag caccgggttc tgcgtgcct gccacggctg cctcttcatt	240
gcctgcttcg tcttggtcct cagcgagagc tccatcttca gtctcctggc catcgccatt	300
gaccgctaca ttgccatccg catcccgctc cggtacaatg gcttggtgac cgggacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcggttg ccatcggcct gactcccatg	420
ctaggttga acaactgagg tcagccaaag gagggcaaga accactcca gggctgcggg	480
gagggccaag tggcctgtct ctttgaggat gtgggtccca tgaactacat ggtgtacttc	540
aacttctttg cctgtgtgct ggtgcccctg ctgctcatgc tgggtgtcta tttgcggatc	600
ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgtcc ggggtgttgt	660
gcacgggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg	720
ctctttgccc tctgctggct gcccctacac atcatcaact gcttcacttt cttctgcccc	780
gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat	840
tcggttgtga atcccttcat ctacgcctac cgtatccgag agttccgcca gaccttccgc	900
aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt	960
gcccgggtct tggcagctca tggcagtgac ggagagcagg tcagcctccg tctcaacggt	1020
gtgagcaagg gcgaggagct gttcaccggg gtgggtgcca tctggtcga gctggacggc	1080
gacgtaaacy gccacaggtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc	1140
aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gccaccctc	1200

gtgaccaccc tgacctgggg cgtgcagtgc ttcagccgct accccgacca catgaagcag 1260
cacgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgtac catcttcttc 1320
aaggacgacg gcaactacaa gacccgcgcc gaggtgaagt tcgagggcga caccctggtg 1380
aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 1440
ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc 1500
atcaaggccc acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 1560
cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgcccga caaccactac 1620
ctgagcaccc agtccgccct gagcaaagac cccaacgaga agcgcgatca catggtcctg 1680
ctggagttcg tgaccgccgc cgggatcact ctcggcattg acgagctgta caagtaa 1737

<210> 40

<211> 578

<212> PRT

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C49 amino acid sequence

<400> 40

Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1 5 10 15

Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
195 200 205

Lys Gln Met Glu Ser Gln Cys Cys Pro Gly Cys Cys Ala Arg Ser Thr
210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr
275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg
290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser
305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu
325 330 335

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
340 345 350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser
355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
420 425 430

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
435 440 445

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
565 570 575

Tyr Lys

<210> 41

<211> 1686

<212> DNA

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C33 cDNA sequence

<400> 41

atgcccatca tgggctcctc ggtgtacatc acggtggagc tggccattgc tgtgctggcc	60
atcctgggca atgtgctggt gtgctgggcc gtgtggctca acagcaacct gcagaacgtc	120
accaactact ttgtggtgtc actggcggcg gccgacatcg cagtgggtgt gctcgccatc	180
ccctttgcc a tcaccatcag caccgggttc tgcgtgcct gccacggctg cctcttcatt	240
gcctgcttcg tcttggtcct cacgcagagc tccatcttca gtctcctggc catcgccatt	300
gaccgctaca ttgccatccg catcccgtc cgggtacaatg gcttggtgac cgggacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg	420
ctaggttgga acaactgcgg tcagccaaag gagggcaaga accactcca gggctgcggg	480
gagggccaaag tggcctgtct ctttgaggat gtgggtccca tgaactacat ggtgtacttc	540
aacttctttg cctgtgtgct ggtgcccctg ctgctcatgc tgggtgtcta tttgcggatc	600
ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agtgttgtcc ggggtgttgt	660
gcacggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg	720
ctctttgccc tctgctggct gccctacac atcatcaact gtttcacttt cttctgcccc	780
gactgcagcc acgcccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat	840
tcggttgtga atcccttcat ctacgcctac cgtatccgcg agttccgcca gaccttccgc	900

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aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt      960
gcccgggtcg tgagcaaggg cgaggagctg ttcaccgggg tggtgcccat cctgggtcgag    1020
ctggacggcg acgtaaacgg ccacaggttc agcgtgtccg gcgagggcga gggcgatgcc      1080
acctacggca agctgaccct gaagttcacg tgcaccaccg gcaagctgcc cgtgccctgg      1140
cccaccctcg tgaccaccct gacctggggc gtgcagtgtc tcagccgcta ccccgaccac      1200
atgaagcagc acgacttctt caagtccgcc atgccgaag gctacgtcca ggagcgtacc      1260
atctttcttca aggacgacgg caactacaag acccgcgccg aggtgaagtt cgagggcgac      1320
accctggtga accgcatcga gctgaagggc atcgacttca aggaggacgg caacatcctg      1380
gggcacaagc tggagtacaa ctacatcagc cacaacgtct atatcaccgc cgacaagcag      1440
aagaacggca tcaaggccca cttcaagatc cgccacaaca tcgaggacgg cagcgtgcag      1500
ctcgccgacc actaccagca gaacaccccc atcggcgacg gccccgtgct gctgcccgac      1560
aaccactacc tgagcaccca gtccgccctg agcaaagacc ccaacgagaa gcgcgatcac      1620
atggtcctgc tggagtctgt gaccgccgcc gggatcactc tcggcatgga cgagctgtac      1680
aagtaa                                           1686

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<210> 42

<211> 561

<212> PRT

<213> artificial sequence

<220>

<223> A2A-FlashPG-CFP-C33 amino acid sequence

<400> 42

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Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1           5           10          15

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Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
          20           25           30

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Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
          35           40           45

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Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
195 200 205

Lys Gln Met Glu Ser Gln Cys Cys Pro Gly Cys Cys Ala Arg Ser Thr
210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr

275		280		285
Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg				
290		295		300
Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser				
305		310		315 320
Ala Arg Val Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val Pro				
	325		330	335
Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser Val				
	340		345	350
Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu Lys				
	355		360	365
Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu Val				
	370		375	380
Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp His				
385		390		395 400
Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr Val				
	405		410	415
Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr Arg				
	420		425	430
Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu Leu				
	435		440	445
Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys Leu				
	450		455	460
Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys Gln				
465		470		475 480
Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu Asp				
	485		490	495
Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile Gly				
	500		505	510

Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln Ser
515 520 525

Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu Leu
530 535 540

Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu Tyr
545 550 555 560

Lys

<210> 43

<211> 1788

<212> DNA

<213> artificial sequence

<220>

<223> A2A-CFP-ModelPG-C49 cDNA sequence

<400> 43

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accaactact ttgtggtgtc actggcgggc gccgacatcg cagtgggtgt gctcgccatc	180
ccctttgcc taccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt	240
gcctgcttcg tcttggctct cacgcagagc tccatcttca gtctcctggc catcgccatt	300
gaccgctaca ttgccatccg catcccgtc cggtacaatg gcttggtgac cggcacgagg	360
gctaagggca tcattgccat ctgctgggtg ctgtcgtttg ccatcggcct gactcccatg	420
ctagggttga acaactgcgg tcagccaaag gagggcaaga accactcca gggctgcggg	480
gagggccaag tggcctgtct ctttgaggat gtgggtccca tgaactacat ggtgtacttc	540
aacttctttg cctgtgtgct ggtgccctg ctgctcatgc tgggtgtcta tttgcggatc	600
ttcctggcgg cgcgacgaca gctgaagcag atggagagcc agcctctgcc gggggagcgg	660
gcacggtcca cactgcagaa ggaggtccat gctgccaagt cactggccat cattgtgggg	720

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ctctttgccc tctgctggct gcccctacac atcatcaact gcttcacttt cttctgcccc 780
gactgcagcc acgccccctct ctggctcatg tacctggcca tcgtcctctc ccacaccaat 840
tcggttgtga atcccttcat ctacgcctac cgtatccgcg agttccgcca gaccttccgc 900
aagatcattc gcagccacgt cctgaggcag caagaacctt tcaaggcagc tggcaccagt 960
gcccgggtct tggcagctca tggcagtgac ggagagcagg tcagcctccg tctcaacggc 1020
gtgagcaagg gcgaggagct gttcaccggg gtggtgccca tcctggtcga gctggacggc 1080
gacgtaaacy gccacaggtt cagcgtgtcc ggcgagggcg agggcgatgc cacctacggc 1140
aagctgaccc tgaagttcat ctgcaccacc ggcaagctgc ccgtgccctg gccaccctc 1200
gtgaccaccc tgacctgggg cgtgcagtgc ttcagccgct accccgacca catgaagcag 1260
cacgacttct tcaagtccgc catgcccga ggctacgtcc aggagcgtac catcttcttc 1320
aaggacgacg gcaactacaa gaccgcgcc gaggtgaagt tcgagggcga caccctggtg 1380
aaccgcatcg agctgaaggg catcgacttc aaggaggacg gcaacatcct ggggcacaag 1440
ctggagtaca actacatcag ccacaacgtc tatatcaccg ccgacaagca gaagaacggc 1500
atcaaggccc acttcaagat ccgccacaac atcgaggacg gcagcgtgca gctcgccgac 1560
cactaccagc agaacacccc catcggcgac ggccccgtgc tgctgccga caaccactac 1620
ctgagcacc agtccgcctt gagcaaagac cccaacgaga agcgcgatca catggtcctg 1680
ctggagttcg tgaccgccgc cgggatcact ctcggcattg acgagctgta caaggctgag 1740
gctgcagcgc gcgaagcatg ctgcccaggt tgttgcgctc gcgcatga 1788

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<210> 44

<211> 595

<212> PRT

<213> artificial sequence

<220>

<223> A2A-CFP-ModelPG-C49 amino acid sequence

<400> 44

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Met Pro Ile Met Gly Ser Ser Val Tyr Ile Thr Val Glu Leu Ala Ile
1           5           10          15

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Ala Val Leu Ala Ile Leu Gly Asn Val Leu Val Cys Trp Ala Val Trp
20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
195 200 205

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr
210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr

245	250	255
Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu		
260	265	270
Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr		
275	280	285
Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg		
290	295	300
Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser		
305	310	315
Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu		
325	330	335
Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val		
340	345	350
Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser		
355	360	365
Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu		
370	375	380
Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu		
385	390	395
Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp		
405	410	415
His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr		
420	425	430
Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr		
435	440	445
Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu		
450	455	460
Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys		
465	470	475
		480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
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Tyr Lys Ala Glu Ala Ala Ala Arg Glu Ala Cys Cys Pro Gly Cys Cys
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Ala Arg Ala
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<220>

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accaactact ttgtggtgtc actggcgggc gccgacatcg cagtgggtgt gctcgccatc 180
ccctttgccca tcaccatcag caccgggttc tgcgctgcct gccacggctg cctcttcatt 240

gectgcttcg tectggctct cacgcagagc tccatcttca gtctcctggc catcgccatt	300
gaccgctaca ttgccatccg catcccgtc cgggtacaatg gcttggtgac cggcacgagg	360
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<212> PRT

<213> artificial sequence

<220>

<223> A2A-CFP-C49 amino acid sequence

<400> 46

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20 25 30

Leu Asn Ser Asn Leu Gln Asn Val Thr Asn Tyr Phe Val Val Ser Leu
35 40 45

Ala Ala Ala Asp Ile Ala Val Gly Val Leu Ala Ile Pro Phe Ala Ile
50 55 60

Thr Ile Ser Thr Gly Phe Cys Ala Ala Cys His Gly Cys Leu Phe Ile
65 70 75 80

Ala Cys Phe Val Leu Val Leu Thr Gln Ser Ser Ile Phe Ser Leu Leu
85 90 95

Ala Ile Ala Ile Asp Arg Tyr Ile Ala Ile Arg Ile Pro Leu Arg Tyr
100 105 110

Asn Gly Leu Val Thr Gly Thr Arg Ala Lys Gly Ile Ile Ala Ile Cys
115 120 125

Trp Val Leu Ser Phe Ala Ile Gly Leu Thr Pro Met Leu Gly Trp Asn
130 135 140

Asn Cys Gly Gln Pro Lys Glu Gly Lys Asn His Ser Gln Gly Cys Gly
145 150 155 160

Glu Gly Gln Val Ala Cys Leu Phe Glu Asp Val Val Pro Met Asn Tyr
165 170 175

Met Val Tyr Phe Asn Phe Phe Ala Cys Val Leu Val Pro Leu Leu Leu
180 185 190

Met Leu Gly Val Tyr Leu Arg Ile Phe Leu Ala Ala Arg Arg Gln Leu
195 200 205

Lys Gln Met Glu Ser Gln Pro Leu Pro Gly Glu Arg Ala Arg Ser Thr
210 215 220

Leu Gln Lys Glu Val His Ala Ala Lys Ser Leu Ala Ile Ile Val Gly
225 230 235 240

Leu Phe Ala Leu Cys Trp Leu Pro Leu His Ile Ile Asn Cys Phe Thr
245 250 255

Phe Phe Cys Pro Asp Cys Ser His Ala Pro Leu Trp Leu Met Tyr Leu
260 265 270

Ala Ile Val Leu Ser His Thr Asn Ser Val Val Asn Pro Phe Ile Tyr
275 280 285

Ala Tyr Arg Ile Arg Glu Phe Arg Gln Thr Phe Arg Lys Ile Ile Arg
290 295 300

Ser His Val Leu Arg Gln Gln Glu Pro Phe Lys Ala Ala Gly Thr Ser
305 310 315 320

Ala Arg Val Leu Ala Ala His Gly Ser Asp Gly Glu Gln Val Ser Leu
325 330 335

Arg Leu Asn Gly Val Ser Lys Gly Glu Glu Leu Phe Thr Gly Val Val
340 345 350

Pro Ile Leu Val Glu Leu Asp Gly Asp Val Asn Gly His Arg Phe Ser
355 360 365

Val Ser Gly Glu Gly Glu Gly Asp Ala Thr Tyr Gly Lys Leu Thr Leu
370 375 380

Lys Phe Ile Cys Thr Thr Gly Lys Leu Pro Val Pro Trp Pro Thr Leu
385 390 395 400

Val Thr Thr Leu Thr Trp Gly Val Gln Cys Phe Ser Arg Tyr Pro Asp
405 410 415

His Met Lys Gln His Asp Phe Phe Lys Ser Ala Met Pro Glu Gly Tyr
420 425 430

Val Gln Glu Arg Thr Ile Phe Phe Lys Asp Asp Gly Asn Tyr Lys Thr
435 440 445

Arg Ala Glu Val Lys Phe Glu Gly Asp Thr Leu Val Asn Arg Ile Glu
450 455 460

Leu Lys Gly Ile Asp Phe Lys Glu Asp Gly Asn Ile Leu Gly His Lys
465 470 475 480

Leu Glu Tyr Asn Tyr Ile Ser His Asn Val Tyr Ile Thr Ala Asp Lys
485 490 495

Gln Lys Asn Gly Ile Lys Ala His Phe Lys Ile Arg His Asn Ile Glu
500 505 510

Asp Gly Ser Val Gln Leu Ala Asp His Tyr Gln Gln Asn Thr Pro Ile
515 520 525

Gly Asp Gly Pro Val Leu Leu Pro Asp Asn His Tyr Leu Ser Thr Gln
530 535 540

Ser Ala Leu Ser Lys Asp Pro Asn Glu Lys Arg Asp His Met Val Leu
545 550 555 560

Leu Glu Phe Val Thr Ala Ala Gly Ile Thr Leu Gly Met Asp Glu Leu
565 570 575

Tyr Lys

50/66

51/66